



-1-

SEQUENCE LISTING

<110> EISAI CO., LTD.

<120> ADIP PROTEIN AND USE THEREOF

<130> 2144.0100000

<140> US 10/644,084

<141> 2003-08-20

<150> JP 2002-284263

<151> 2002-09-27

<160> 9

<170> PatentIn version 3.3

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<220>

<221> CDS

<222> (80)..(1927)

<223> /note="afadin-and alpha-actinin-binding protein"

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Met Gly Asp Trp Met Thr Val Thr Asp Pro Val

1

5

10

ctg tgt aca gaa aac aaa aat ctc tct caa tat acc tca gaa aca aag 160

Leu Cys Thr Glu Asn Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys

15

20

25

atg tct ccg tcc agt ttg tac tcc cag caa gtt ctg tgc tct tca gta	208	
Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val		
30	35	40
cct tta tcc aaa aac gtg cat ggt gtt ttc ggt gtc ttc tgc aca gga	256	
Pro Leu Ser Lys Asn Val His Gly Val Phe Gly Val Phe Cys Thr Gly		
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gag aac att gaa caa agt att tcc tat ctt gat cag gag ctg acc acc	304	
Glu Asn Ile Glu Gln Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr		
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ttc ggg ttt cct tcc ttg tat gaa gaa tcc aaa agt aaa gag gca aag	352	
Phe Gly Phe Pro Ser Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys		
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aga gaa tta aat ata gtc gct gtt ctg aac tgt atg aac gag ctg ctc	400	
Arg Glu Leu Asn Ile Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu		
95	100	105
gtg ctt cag cgg aag aac ctg ctg gcc cag gag agc gtg gag aca cag	448	
Val Leu Gln Arg Lys Asn Leu Ala Gln Glu Ser Val Glu Thr Gln		
110	115	120
aac ttg aag ctg ggc agt gac atg gac cac ctg cag agc tgc tac gcc	496	
Asn Leu Lys Leu Gly Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala		
125	130	135
aaa ctt aag gag cag ttg gaa acg tcc agg cgg gag atg atc ggg ctt	544	
Lys Leu Lys Glu Gln Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu		
140	145	150
155		
caa gag aga gac agg cag ctg cag tgc aag aac agg agt ttg cat cag	592	
Gln Glu Arg Asp Arg Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln		
160	165	170
ctc ctg aag aat gag aaa gat gag gta caa aaa tta caa aat atc ata	640	
Leu Leu Lys Asn Glu Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile		
175	180	185

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Ala	Ser	Arg	Ala	Thr	Gln	Tyr	Asn	His	Asp	Val	Lys	Arg	Lys	Glu	Arg	
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gaa	tat	aat	aag	cta	aag	gag	cgc	ctg	cat	cag	ctc	gtt	atg	aac	aag	736
Glu	Tyr	Asn	Lys	Leu	Lys	Glu	Arg	Leu	His	Gln	Leu	Val	Met	Asn	Lys	
205					210						215					
aag	gat	aaa	aac	ata	gcc	atg	gat	gtt	tta	aat	tat	gtg	ggt	cga	gct	784
Lys	Asp	Lys	Asn	Ile	Ala	Met	Asp	Val	Leu	Asn	Tyr	Val	Gly	Arg	Ala	
220					225					230				235		
gat	ggc	aaa	cga	ggc	tca	tgg	agg	act	gac	aaa	aca	gaa	gcc	agg	aat	832
Asp	Gly	Lys	Arg	Gly	Ser	Trp	Arg	Thr	Asp	Lys	Thr	Glu	Ala	Arg	Asn	
240					245					250						
gaa	gat	gag	atg	tac	aaa	att	ctg	ttg	aat	gat	tat	gag	tac	cgc	cag	880
Glu	Asp	Glu	Met	Tyr	Lys	Ile	Leu	Leu	Asn	Asp	Tyr	Glu	Tyr	Arg	Gln	
255					260					265						
aag	cag	atc	ctg	atg	gag	aac	gcg	gag	ctg	aag	aag	gtc	ctc	cag	cag	928
Lys	Gln	Ile	Leu	Met	Glu	Asn	Ala	Glu	Leu	Lys	Lys	Val	Leu	Gln	Gln	
270					275					280						
atg	aag	aag	gag	atg	atc	tct	ctc	ctg	tct	cct	cag	aag	aag	ccc	976	
Met	Lys	Glu	Met	Ile	Ser	Leu	Leu	Ser	Pro	Gln	Lys	Lys	Lys	Pro		
285					290					295						
agg	gaa	aga	gca	gag	gac	ggc	aca	ggc	act	gtt	gct	atc	tcc	gat	ata	1024
Arg	Glu	Arg	Ala	Glu	Asp	Gly	Thr	Gly	Thr	Val	Ala	Ile	Ser	Asp	Ile	
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gaa	gat	gac	tct	ggg	gaa	ctg	agc	aga	gac	agc	gtg	tgg	ggc	ctt	tcc	1072
Glu	Asp	Asp	Ser	Gly	Glu	Leu	Ser	Arg	Asp	Ser	Val	Trp	Gly	Leu	Ser	
320					325					330						
tgt	gac	act	gtg	aga	gag	cag	ctg	aca	aac	agc	atc	agg	aaa	cag	tgg	1120
Cys	Asp	Thr	Val	Arg	Glu	Gln	Leu	Thr	Asn	Ser	Ile	Arg	Lys	Gln	Trp	
335					340					345						

aga att ttg aaa agt cat gta gaa aaa ctc gat aac caa gct tcg aag	350	355	360	1168
Arg Ile Leu Lys Ser His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys				
gta cac tca gag ggc ctt aat gag gag gac gtc atc tca cga caa gac	365	370	375	1216
Val His Ser Glu Gly Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp				
cat gag caa gag act gag aaa ctg gag ctg gag att gag cggttgtaaa	380	385	390	1264
His Glu Gln Glu Thr Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys				
gag atg atc aag gct cag cag cag ctc tta cag cag cag ctg gcc acc	400	405	410	1312
Glu Met Ile Lys Ala Gln Gln Leu Leu Gln Gln Leu Ala Thr				
acg tgt gat gat gac acc acc tca ctg ttg cga gac tgt tac ttg ctg	415	420	425	1360
Thr Cys Asp Asp Asp Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu				
gaa gaa aag gaa cgc ctt aaa gaa gag tgg acc ctt ttt aaa gag caa	430	435	440	1408
Glu Glu Lys Glu Arg Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln				
aaa aag aat ttt gag aga gaa agg cga agc ttt aca gaa gct gcc att	445	450	455	1456
Lys Lys Asn Phe Glu Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile				
cga ttg ggg ttg gag aga aag gcg ttt gaa gaa gag cga gcc agc tgg	460	465	470	1504
Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp				
gta aag cag cag ttt tta aac atg acg aac ttt gac cac cag aac tca	480	485	490	1552
Val Lys Gln Gln Phe Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser				
gaa aat gtg aaa ctt ttc agt gcc ttc tca gga agt tct gat cca gac	495	500	505	1600
Glu Asn Val Lys Leu Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp				

aat ctt ata gtc cac tca cg ^g cca cg ^g caa aag aag cta cac agt gt ^g	1648		
Asn Leu Ile Val His Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val			
510	515	520	
gct aat ggg gt ^g cca gct tgc aca tca aaa ct ^g act aaa tct ctt cct	1696		
Ala Asn Gly Val Pro Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro			
525	530	535	
gcc tca cct tct act tca gac ttt cg ^c cag aca cat tca tgt gt ^g tct	1744		
Ala Ser Pro Ser Thr Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser			
540	545	550	555
gaa cac agt tcc atc agt gt ^g ct ^g aat ata act cct gaa gaa agt aaa	1792		
Glu His Ser Ser Ile Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys			
560	565	570	
cca agt gag gtt gca aga gaa agc acg gat cag aag tgg agc gt ^g cag	1840		
Pro Ser Glu Val Ala Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln			
575	580	585	
tcg agg ccc agc tcg cg ^g gag ggg tgc tac agc gga tgc tcc tcg gcc	1888		
Ser Arg Pro Ser Ser Arg Glu Gly Cys Tyr Ser Gly Cys Ser Ser Ala			
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ttc agg agc gct cac ggg gac cga gat gac tta cct taa atgtgcgggc	1937		
Phe Arg Ser Ala His Gly Asp Arg Asp Asp Leu Pro			
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tgcagtgc ^t g ttcccagatg tg ^c gc ^t tagag gagttgacac agggtgtac ataaagt ^c ag	1997		
tcgtctaact taagatgctc agagttgttt gttggactt cgctgtcttc ccccaaagag	2057		
ctgaaaatgct aagctactta aaaggatgca aagcttttgt tgtgtgttag taacagaagc	2117		
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attcg ^t ccca agtgtggttg gcattggaag tgtagcc ^t ttt acttgaatgt atactgt ^a ga	2297		

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Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val Pro Leu Ser Lys Asn
35 40 45

Val His Gly Val Phe Gly Val Phe Cys Thr Gly Glu Asn Ile Glu Gln
50 55 60

Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser
65 70 75 80

Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys Arg Glu Leu Asn Ile
85 90 95

Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys
100 105 110

Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln Asn Leu Lys Leu Gly
115 120 125

Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala Lys Leu Lys Glu Gln
130 135 140

Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu Gln Glu Arg Asp Arg
145 150 155 160

Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln Leu Leu Lys Asn Glu
165 170 175

Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr
180 185 190

Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu
195 200 205

Lys Glu Arg Leu His Gln Leu Val Met Asn Lys Lys Asp Lys Asn Ile
210 215 220

Ala Met Asp Val Leu Asn Tyr Val Gly Arg Ala Asp Gly Lys Arg Gly
225 230 235 240

Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr
245 250 255

Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Met
260 265 270

Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln Met Lys Lys Glu Met
275 280 285

Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro Arg Glu Arg Ala Glu
290 295 300

Asp Gly Thr Gly Thr Val Ala Ile Ser Asp Ile Glu Asp Asp Ser Gly
305 310 315 320

Glu Leu Ser Arg Asp Ser Val Trp Gly Leu Ser Cys Asp Thr Val Arg
325 330 335

Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser
340 345 350

His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys Val His Ser Glu Gly
355 360 365

Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr
370 375 380

Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys Glu Met Ile Lys Ala
385 390 395 400

Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr Thr Cys Asp Asp Asp
405 410 415

Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg
420 425 430

Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu
435 440 445

Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu
450 455 460

Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp Val Lys Gln Gln Phe
465 470 475 480

Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu
485 490 495

Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp Asn Leu Ile Val His
500 505 510

Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val Ala Asn Gly Val Pro
515 520 525

Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro Ala Ser Pro Ser Thr
530 535 540

Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser Glu His Ser Ser Ile
545 550 555 560

Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys Pro Ser Glu Val Ala
565 570 575

Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln Ser Arg Pro Ser Ser
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Gly Asp Arg Asp Asp Leu Pro
610 615

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Met Gly Asp Trp Met Thr Val Thr Asp Pro Val
1 5 10

ctg tgt aca gaa aac aaa aat ctc tct caa tat acc tca gaa aca aag			159
Leu Cys Thr Glu Asn Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys			
15	20	25	
atg tct ccg tca agt tta tac tcg cag caa gta ctg tgc tct gca aca			207
Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ala Thr			
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Pro Leu Ser Lys Asn Val His Gly Val Phe Ser Ala Phe Cys Thr Gly			
45	50	55	
gag aac atc gaa cag agt att tcg tat ctt gat cag gaa ctg act acc			303
Glu Asn Ile Glu Gln Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr			
60	65	70	75
ttc ggt ttc cct tcc ttg tat gaa gaa tcc aaa agt aag gag gcg aag			351
Phe Gly Phe Pro Ser Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys			
80	85	90	
cga gag tta agt ata gtt gct ctt ctg aac tgc atg aat gag ctg ctt			399
Arg Glu Leu Ser Ile Val Ala Leu Leu Asn Cys Met Asn Glu Leu Leu			
95	100	105	
gtg ctt cag cgg aag aac ctc ctg gcc cag gaa agc gtg gag aca cag			447
Val Leu Gln Arg Lys Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln			
110	115	120	
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Asn Leu Lys Leu Gly Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala			
125	130	135	
aaa ctt aag gaa cag ttg gag gcc tcc agg cga gag atg atc agc ctt			543
Lys Leu Lys Glu Gln Leu Glu Ala Ser Arg Arg Glu Met Ile Ser Leu			
140	145	150	155
cag gag aga gac aga cag cta cag tgc aaa aac agg aat ttg cat cag			591
Gln Glu Arg Asp Arg Gln Leu Gln Cys Lys Asn Arg Asn Leu His Gln			
160	165	170	

ctc ctg aaa aac gag aaa gaa gag gta caa aaa tta caa aat atc ata			639
Leu Leu Lys Asn Glu Lys Glu Glu Val Gln Lys Leu Gln Asn Ile Ile			
175	180	185	
gcc agt cgg gct act cag tat aat cat gat gtg aag aga aag gag cgg			687
Ala Ser Arg Ala Thr Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg			
190	195	200	
gag tac aat aaa ctg aag gag cgt ctg cat cag ctt gtt atg aac aag			735
Glu Tyr Asn Lys Leu Lys Glu Arg Leu His Gln Leu Val Met Asn Lys			
205	210	215	
aag gat aaa aat ata gcc atg gac gtt tta aat tac gtg ggc cga gtg			783
Lys Asp Lys Asn Ile Ala Met Asp Val Leu Asn Tyr Val Gly Arg Val			
220	225	230	235
gat gga aag cga ggc tcc tgg agg act gat aaa aca gaa gcc agg aat			831
Asp Gly Lys Arg Gly Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn			
240	245	250	
gaa gat gaa atg tac aaa att ctg ctg aat gat tat gag tac cgc cag			879
Glu Asp Glu Met Tyr Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln			
255	260	265	
aag cag atc ctg ctg gag aat gcg gag ctg aag aag gtc ctc cag cag			927
Lys Gln Ile Leu Leu Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln			
270	275	280	
atg aag aaa gag atg atc tct ctc ctt tct cct caa aag aag aaa ccc			975
Met Lys Lys Glu Met Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro			
285	290	295	
aga gaa aga gca gag gac agc aca ggc act gtt gtc atc tcc gat gta			1023
Arg Glu Arg Ala Glu Asp Ser Thr Gly Thr Val Val Ile Ser Asp Val			
300	305	310	315
gaa gac gac gct ggg gag ctg agc aga gat ggt gtg tgg agc ctt tcc			1071
Glu Asp Asp Ala Gly Glu Leu Ser Arg Asp Gly Val Trp Ser Leu Ser			
320	325	330	

tgt gac act gtc agg gag cag ctt aca aac agc atc agg aag cag tgg			1119
Cys Asp Thr Val Arg Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp			
335	340	345	
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Arg Ile Leu Lys Ser His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys			
350	355	360	
gta cac tca gag ggc ttt cat gaa gag gac gtc atc tca cga caa gac			1215
Val His Ser Glu Gly Phe His Glu Glu Asp Val Ile Ser Arg Gln Asp			
365	370	375	
cat gag caa gag act gag aaa ctg gag ctg gag att gag cgg tgt aaa			1263
His Glu Gln Glu Thr Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys			
380	385	390	395
gag atg atc aag gct cag cag ctc tta cag caa cag ctg gcc act			1311
Glu Met Ile Lys Ala Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr			
400	405	410	
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Ala Cys Asp Asp Asp Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu			
415	420	425	
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430	435	440	
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445	450	455	
cgc ttg ggg ttg gag aga aag gcg ttt gag gaa gag cga gcc agc tgg			1503
Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp			
460	465	470	475
gtg aag cag cag ttt tta aac atg acg acc ttt gat cac cag aac tca			1551
Val Lys Gln Gln Phe Leu Asn Met Thr Thr Phe Asp His Gln Asn Ser			
480	485	490	

gaa aat gtg aaa ctt ttc agt gcc ttt tca gga agt tct gat cca gac	495	500	505	1599
Glu Asn Val Lys Leu Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp				
aat ctt ata gtc cac cca cg ^g cca cg ^g caa aag aag cca cac agt gtc	510	515	520	1647
Asn Leu Ile Val His Pro Arg Pro Arg Gln Lys Lys Pro His Ser Val				
gct aat ggg gtg cca gct tgc aca tcc aaa ctg gct aag tct ctt cc ^g	525	530	535	1695
Ala Asn Gly Val Pro Ala Cys Thr Ser Lys Leu Ala Lys Ser Leu Pro				
acc tca cct tca gac ttc tgc cc ^g tct cg ^c tca tgt gtg tct gag cac	540	545	550	1743
Thr Ser Pro Ser Asp Phe Cys Pro Ser Arg Ser Cys Val Ser Glu His				
agt ccc gtc agt gc ^g ctg act gtg act cct gaa gaa acc aaa cc ^g aat	560	565	570	1791
Ser Pro Val Ser Ala Leu Thr Val Thr Pro Glu Glu Thr Lys Pro Asn				
gag gtt gga aga gaa agt acg gac cag aag tgg agc gtg gtg tcc aga	575	580	585	1839
Glu Val Gly Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Val Ser Arg				
ccc agc tcc cg ^g gag ggt tgc tac ggt gga tgc tcc tc ^g gcc tac aca	590	595	600	1887
Pro Ser Ser Arg Glu Gly Cys Tyr Gly Gly Cys Ser Ser Ala Tyr Thr				
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Ser Ser His Val Glu Arg Asp Asp Leu Pro				
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acactctgga	cactggtg	ttgttcattt	ctagaacaat	cgtaggctct	tttctctgtt	2960
tctgctgcat	gtttcttcatt	gagaagtatg	ttactattga	cagtaatgac	actgacagtg	3020
actgttagacg	taggcccaga	cttctcctgg	gtggattttc	atccagcagc	ttttaagtgc	3080
ctcgccctgc	tcgtctctgc	acatagccgc	cgacacaagc	cctcgcttga	tgtgcagat	3140
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<211> 613

<212> PRT

<213> Rattus norvegicus

<400> 4

Met Gly Asp Trp Met Thr Val Thr Asp Pro Val Leu Cys Thr Glu Asn
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Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys Met Ser Pro Ser Ser
20 25 30

Leu Tyr Ser Gln Gln Val Leu Cys Ser Ala Thr Pro Leu Ser Lys Asn
35 40 45

Val His Gly Val Phe Ser Ala Phe Cys Thr Gly Glu Asn Ile Glu Gln
50 55 60

Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser
65 70 75 80

Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys Arg Glu Leu Ser Ile
85 90 95

Val Ala Leu Leu Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys
100 105 110

Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln Asn Leu Lys Leu Gly
115 120 125

Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala Lys Leu Lys Glu Gln
130 135 140

Leu Glu Ala Ser Arg Arg Glu Met Ile Ser Leu Gln Glu Arg Asp Arg
145 150 155 160

Gln Leu Gln Cys Lys Asn Arg Asn Leu His Gln Leu Leu Lys Asn Glu
165 170 175

Lys Glu Glu Val Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr
180 185 190

Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu
195 200 205

Lys Glu Arg Leu His Gln Leu Val Met Asn Lys Lys Asp Lys Asn Ile
210 215 220

Ala Met Asp Val Leu Asn Tyr Val Gly Arg Val Asp Gly Lys Arg Gly
225 230 235 240

Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr
245 250 255

Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Leu
260 265 270

Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln Met Lys Lys Glu Met
275 280 285

Ile Ser Leu Leu Ser Pro Gln Lys Lys Pro Arg Glu Arg Ala Glu
290 295 300

Asp Ser Thr Gly Thr Val Val Ile Ser Asp Val Glu Asp Asp Ala Gly
305 310 315 320

Glu Leu Ser Arg Asp Gly Val Trp Ser Leu Ser Cys Asp Thr Val Arg
 325 330 335

Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser
 340 345 350

His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys Val His Ser Glu Gly
 355 360 365

Phe His Glu Glu Asp Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr
 370 375 380

Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys Glu Met Ile Lys Ala
385 390 395 400

Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr Ala Cys Asp Asp Asp
 405 410 415

Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg
420 425 430

Leu Lys Glu Glu Trp Ser Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu
435 440 445

Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu
450 455 460

Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp Val Lys Gln Gln Phe
465 470 475 480

Leu Asn Met Thr Thr Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu
485 490 495

Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp Asn Leu Ile Val His
500 505 510

Pro Arg Pro Arg Gln Lys Lys Pro His Ser Val Ala Asn Gly Val Pro
515 520 525

Ala Cys Thr Ser Lys Leu Ala Lys Ser Leu Pro Thr Ser Pro Ser Asp
530 535 540

Phe Cys Pro Ser Arg Ser Cys Val Ser Glu His Ser Pro Val Ser Ala
545 550 555 560

Leu Thr Val Thr Pro Glu Glu Thr Lys Pro Asn Glu Val Gly Arg Glu
565 570 575

Ser Thr Asp Gln Lys Trp Ser Val Val Ser Arg Pro Ser Ser Arg Glu
580 585 590

Gly Cys Tyr Gly Gly Cys Ser Ser Ala Tyr Thr Ser Ser His Val Glu
595 600 605

Arg Asp Asp Leu Pro
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<211> 22

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 5

cgttaggagag tgacaggagc tg

22

<210> 6

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 6

ggttatcgag ttttctaca tgac

24

<210> 7

<211> 22

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 7

cgttaggagag tgacaggagc tg

22

<210> 8

<211> 23

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 8

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23

<210> 9

<211> 626

<212> PRT

<213> Homo sapiens

<400> 9

Thr Ser Ser Ser Gly Ile Leu Ala Leu Glu Ile Ala Met Gly Asp Trp
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Met Thr Val Thr Asp Pro Gly Leu Ser Ser Glu Ser Lys Thr Ile Ser
20 25 30

Gln Tyr Thr Ser Glu Thr Lys Met Ser Pro Ser Ser Leu Tyr Ser Gln
35 40 45

Gln Val Leu Cys Ser Ser Ile Pro Leu Ser Lys Asn Val His Ser Phe
50 55 60

Phe Ser Ala Phe Cys Thr Glu Asp Asn Ile Glu Gln Ser Ile Ser Tyr
65 70 75 80

Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser Leu Tyr Glu Glu
85 90 95

Ser Lys Gly Lys Glu Thr Lys Arg Glu Leu Asn Ile Val Ala Val Leu
100 105 110

Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys Asn Leu Leu Ala
115 120 125

Gln Glu Asn Val Glu Thr Gln Asn Leu Lys Leu Gly Ser Asp Met Asp
130 135 140

His Leu Gln Ser Cys Tyr Ser Lys Leu Lys Glu Gln Leu Glu Thr Ser
145 150 155 160

Arg Arg Glu Met Ile Gly Leu Gln Glu Arg Asp Arg Gln Leu Gln Cys
165 170 175

Lys Asn Arg Asn Leu His Gln Leu Leu Lys Asn Glu Lys Asp Glu Val
180 185 190

Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr Gln Tyr Asn His
195 200 205

Asp Met Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu Lys Glu Arg Leu
210 215 220

His Gln Leu Val Met Asn Lys Lys Asp Lys Lys Ile Ala Met Asp Ile
225 230 235 240

Leu Asn Tyr Val Gly Arg Ala Asp Gly Lys Arg Gly Ser Trp Arg Thr
245 250 255

Gly Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr Lys Ile Leu Leu
260 265 270

Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Met Glu Asn Ala Glu
275 280 285

Leu Lys Lys Val Leu Gln Gln Met Lys Lys Glu Met Ile Ser Leu Leu
290 295 300

Ser Pro Gln Lys Lys Pro Arg Glu Arg Val Asp Asp Ser Thr Gly
305 310 315 320

Thr Val Ile Ser Asp Val Glu Glu Asp Ala Gly Glu Leu Ser Arg Glu
325 330 335

Ser Met Trp Asp Leu Ser Cys Glu Thr Val Arg Glu Gln Leu Thr Asn
340 345 350

Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser His Val Glu Lys Leu
355 360 365

Asp Asn Gln Val Ser Lys Val His Leu Glu Gly Phe Asn Asp Glu Asp
370 375 380

Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr Glu Lys Leu Glu Leu
385 390 395 400

Glu Ile Gln Gln Cys Lys Glu Met Ile Lys Thr Gln Gln Gln Leu Leu
405 410 415

Gln Gln Gln Leu Ala Thr Ala Tyr Asp Asp Asp Thr Thr Ser Leu Leu
420 425 430

Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg Leu Lys Glu Glu Trp
435 440 445

Ser Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu Arg Glu Arg Arg Ser
450 455 460

Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu Arg Lys Ala Phe Glu
465 470 475 480

Glu Glu Arg Ala Ser Trp Leu Lys Gln Gln Phe Leu Asn Met Thr Thr
485 490 495

Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu Phe Ser Ala Phe Ser
500 505 510

Gly Ser Ser Asp Trp Asp Asn Leu Ile Val His Ser Arg Gln Pro Gln
515 520 525

Lys Lys Pro His Ser Val Ser Asn Gly Ser Pro Val Cys Met Ser Lys
530 535 540

Leu Thr Lys Ser Leu Pro Ala Ser Pro Ser Thr Ser Asp Phe Cys Gln
545 550 555 560

Thr Arg Ser Cys Ile Ser Glu His Ser Ser Ile Asn Val Leu Asn Ile
565 570 575

Thr Ala Glu Glu Ile Lys Pro Asn Gln Val Gly Gly Glu Cys Thr Asn
580 585 590

Gln Lys Trp Ser Val Ala Ser Arg Pro Gly Ser Gln Glu Gly Cys Tyr
595 600 605

Ser Gly Cys Ser Leu Ser Tyr Thr Asn Ser His Val Glu Lys Asp Asp
610 615 620

Leu Pro
625